

# X-Linkage Does Not Account for the Absence of Father–Son Similarity in Plasma Uric Acid Concentrations

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Plasma uric acid concentration aggregates in families, and this similarity has been suggested to be due, in part, to multiple shared genes. Men have higher plasma uric acid concentrations than women and are affected with gout nine times more frequently. Rare forms of hyperuricemia and gout are due to mutations of X-linked genes (HPRT1 and PRPS1). Given these observations, we tested the hypothesis that normal variation in plasma uric acid levels would display a pattern of familial similarity consistent with X-linkage in 892 individuals from 196 obese but otherwise healthy families. As predicted by X-linked inheritance, fathers and sons showed no resemblance in plasma uric acid concentration ( $r = 0.013$ , NS), while all other pairings showed moderate-to-strong familial resemblance (ranging from 0.167,  $P < 0.01$ , parent–offspring to 0.415, sister–sister,  $P < 0.01$ ). We then tested the hypothesis that loci along the X chromosome would influence plasma uric acid concentration. We conducted both single-point and multipoint linkage analyses using 17 X-linked markers spaced at approximately 9 cm intervals to determine whether allele sharing among sibs was related to sib similarity in plasma uric acid concentrations ( $n = 1,100$  sib pairs). We found no regions of the X chromosome that cosegregated with plasma uric acid concentrations ( $P > 0.05$ ). We conclude that variation in genes on the X chromosome contribute little to normal

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## INTRODUCTION

Elevated plasma uric acid concentration (hyperuricemia) precedes the onset of gout. Uric acid is a metabolite of purine catabolism, and renal excretion is the primary route of elimination from the body. Elevated uric acid levels are increased after the ingestion of meat and other foods containing purines and after ingestion of alcohol. In addition to environmental determinants, twin and family studies have demonstrated the importance of shared genes in uric acid concentration [Boyle et al., 1967; Brunner et al., 1971; Dal Colleto et al., 1983; Feinleib et al., 1977; Friedlander et al., 1988; Gulbrandsen et al., 1979; Havlik et al., 1977; Jensen et al., 1965; Kalousdian et al., 1987; Laskarzewski et al., 1983; Morton 1979; Rao et al., 1982; Rice et al., 1990; Stecher et al., 1949; Whitfield and Martin 1983]. An early study suggested that gout is a single-gene disorder with an autosomal dominant mode of inheritance with incomplete penetrance [Stecher et al., 1949]. A reanalysis of these data and subsequent segregation analysis of additional families has determined that gout and hyperuricemia are polygenic rather than monogenic traits [Friedlander et al., 1988; Gulbrandsen et al., 1979; Morton 1979; Rao et al., 1982]. This conclusion is further supported by the variability in metabolic disturbances of uric acid metabolism; no common biochemical abnormality is common to all hyperuricemic or gouty patients [Seegmiller et al., 1963].

Several lines of evidence suggest that some genes involved in uric acid regulation might reside on the X chromosome. First, gout and hyperuricemia are more common in men than women. The average level of uric acid is 1 mg/dl more in men compared to women and almost 95% of patients with gout are male [Bondy and Rosenberg, 1980]. Second, mothers transmit gout to

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sons but fathers rarely do [Stecher et al., 1949]. Third, the patterns of correlations found among opposite-sex twin pairs are consistent with sex-linked inheritance [Whitfield and Martin, 1983]. Finally, rare forms of gout and hyperuricemia are associated with single mutations of X-linked genes (HPRT1 and PRPS1 [Becker et al., 1973; Kelley et al., 1967; Yen et al., 1978]). Common forms of gout and hyperuricemia appear to be determined by multiple genes, and one or more of these genes may reside on the X chromosome.

We tested this hypothesis by examining the pattern of family similarity in plasma uric acid concentrations and conducting quantitative linkage analysis in 892 family members from 196 families using 17 markers from the X chromosome. Some family members studied were obese but otherwise healthy, and families were unselected for a family history of gout or hyperuricemia.

## MATERIALS AND METHODS

### Families

We studied nuclear families ascertained from an ongoing family study at the University of Pennsylvania. Families were selected for study if at least two sibs were obese (one sib body mass index (BMI)  $\geq 40$  and one sib BMI  $\geq 30$ ) and the family contained at least one normal weight sib and one normal weight parent (BMI  $\leq 27$ ) [Price et al., 1998]. The resulting families had a wide range of obese and nonobese phenotypes. We divided four three-generation families into eight nuclear families.

### Anthropometric and Plasma Uric Acid Measures

Subjects were weighed and measured for height without shoes, either in hospital gowns or light street clothing. Weight was measured with an Algen Corp Tri Coastal HS 600 scale to the nearest pound and height was measured with a portable Seritex stadiometer to the nearest 0.25 inch. Blood was drawn by venipuncture after an 8-hr fast and analyzed for plasma uric acid (Corning Clinical Laboratories, Horsham, PA). Each subject answered questions contained on a medical history survey.

### Data Analysis, Descriptive Statistics, Univariate, and Familial Correlations

Descriptive statistics were computed for mothers, fathers, sisters, and brothers. Before analysis of family correlations or linkage analysis, plasma uric values were examined to determine if they covaried with age, sex, or BMI; if so, they were adjusted for these variables using multiple regression. Of the several indices available to adjust for obesity, we selected BMI because it accounted for the most variance in uric acid levels and was available for most subjects. Standardized residuals were used as the phenotype in all subsequent analysis of family similarity and linkage.

The correlation between subject characteristics and plasma uric acid concentrations were computed and examined (SPSS 6.1). Family correlations were com-

puted using the FCOR program contained within the SAGE package (Case Western Reserve University, Cleveland). The reported correlations were computed giving equal weight to pairs.

## DNA Analysis and Genotyping

**DNA preparation.** DNA was isolated from whole blood or immortalized lymphoblastoid cells using the high salt method [Lahiri and Nurnberger, 1991].

**Genotyping.** We selected 17 markers that spanned the X chromosome with an average interval of 9.3 cm and no gap greater than 13.5 cm (see Fig. 1 for the list of markers). PCR was conducted in a 10  $\mu$ l reaction volume using conditions appropriate for the particular marker, using previously described protocols [Lee et al., 1999]. Alleles were scored by two readers, blind to phenotype, and checked for Mendelian incompatibilities using the computer program GENEHUNTER. Any incompatibilities identified in the original films were evaluated for scoring or data entry errors. Markers were rerun as required.

**Data analysis, gene mapping.** To estimate locus order and intermarker distance we used the map distances from the Whitehead Institute (WI) [Dib et al., 1996]. For markers not found in the WI database, we consulted the Genome Database, the Cooperative Human Linkage [Sheffield et al., 1995] database, and the Genetic Location Database [Collins et al., 1996]. (See the Electronic Database Information section for the URLs of these databases.)

We computed two statistics as implemented by MAPMAKER/SIBS version 2.0 [Kruglyak et al., 1996]: the EM algorithm-based Haseman-Elston regression (EMHE) [Haseman and Elston, 1972] and the nonparametric linkage quantitative trait loci analysis (NPL) [Kruglyak and Lander, 1995]. In contrast to the traditional Haseman-Elston regression, the EMHE uses information from the full IBD distribution when computing the regression between IBD and the squared phenotypic difference. NPL employs the Wilcoxon

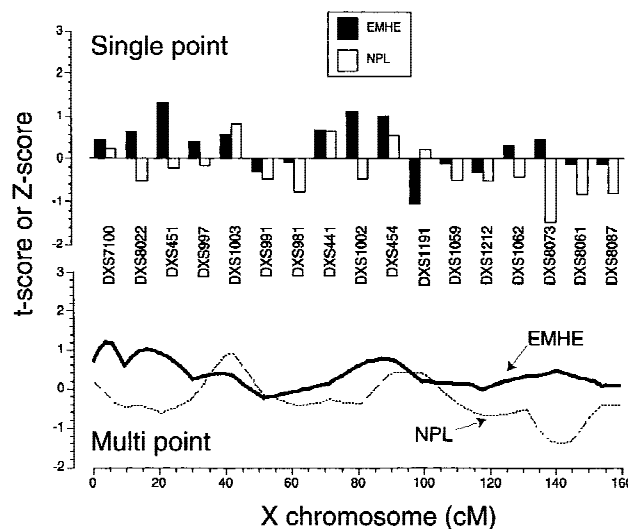


Fig. 1. Single point (upper) and multi point (lower) analysis of plasma uric acid concentration for markers along the X chromosome.

TABLE I. Age, BMI kg/m<sup>2</sup>, Uric Acid Concentration of Family Members

| Relative    | n   | Age (years)    | BMI kg/m <sup>2</sup>  | Uric acid (mg/dl)    |
|-------------|-----|----------------|------------------------|----------------------|
| Mother      | 189 | 65 ± 9 (41–84) | 33.3 ± 9.3 (18.8–65.8) | 5.1 ± 1.6 (1.6–12.9) |
| Father      | 113 | 68 ± 8 (42–86) | 29.3 ± 6.0 (17.3–48.9) | 5.7 ± 1.7 (2.6–14.0) |
| Index cases | 204 | 39 ± 8 (16–61) | 47.6 ± 8.9 (28.8–82.9) | 5.2 ± 1.4 (2.0–9.3)  |
| Sisters     | 347 | 39 ± 8 (17–59) | 34.4 ± 9.9 (18.8–77.6) | 4.4 ± 1.5 (1.4–11.2) |
| Brothers    | 194 | 39 ± 9 (15–65) | 30.9 ± 7.6 (19.7–64.8) | 6.0 ± 1.3 (2.8–8.9)  |

Uric acid values were not available for all family members ( $N_{\text{mothers}} = 161$ ,  $N_{\text{fathers}} = 96$ ,  $N_{\text{index cases}} = 173$ ,  $N_{\text{sisters}} = 302$ ,  $N_{\text{brothers}} = 160$ ).

rank-sum test to evaluate the relation between the rank of absolute phenotypic difference and IBD at a given locus. This approach is robust to assumptions of normality of squared phenotypic differences and lack of correlation between the differences and their residuals. We used all sib pairs in the analysis, and multiple sib pairs within families were weighted by  $\Sigma(N-1)^{-2}$  as suggested by Wilson and Elston [1993]. MAPMAKER/SIBS version 2.0 evaluates both autosomal and X-linked chromosome data; for X-linkage, it is assumed that the difference in phenotype is a function of whether zero or one alleles are inherited identical-by-descent from the mother [Cordell et al., 1995]. Note that parents and sibs providing DNA but without uric acid values were used in the analysis to provide additional information for the computation of identity-by-descent sharing.

## RESULTS

### Subject Characteristics

The parents were in their mid-late 60s and their children were in their late 30s to early 40s (Table I). The average BMI of all groups was over 30 kg/m<sup>2</sup> and ranged from 17.3–82.9 kg/m<sup>2</sup>. Uric acid measurements were obtained on 892 of 1,047 family members (85%). Uric acid levels were, on average, highest in brothers and fathers and lowest in sisters and mothers and ranged from 1.4–14.0 mg/dl. Two individuals reported a previous diagnosis of gout, a father (uric acid 9.8 mg/dl) and a brother from a different family (uric acid 6.3 mg/dl).

Uric acid levels were dependent on sex, age, and BMI kg/m<sup>2</sup> (Table II). The relationships between sex, BMI, and uric acid were consistent for mothers, fathers, index cases, sisters, and brothers, but the effects of age were not the same for each group. There was a negative correlation between age and uric acid levels for some but not all groups; therefore, phenotypes were adjusted

using multivariate regression within sex, generation, and index case categories.

### Familial Aggregation

Plasma uric acid concentrations aggregated in families. There were significant correlations between parent–offspring pairs and among sibs (Table III), with the exception of fathers and their sons. The lack of father–son similarity was not due to the presence of extreme values. When all analyses were conducted eliminating uric acid values greater than 2 SD from the mean, the results were similar to those obtained using all phenotypes (data not shown). Spouse correlations did not differ from zero.

### Gene Mapping Results

Multipoint and single point results for 1,100 sib pairs were in good agreement and both methods of analysis (EMHE and NPL) yielded similar results (Fig. 1). The highest t- or Z-score barely exceeded 1.0 for only one marker for the single-point analyses and a different marker for the multipoint analyses.

## DISCUSSION

Plasma uric acid levels aggregated within families, with the exception of father–son pairs, which showed no similarity in plasma uric acid levels. While this observation might be explained by the absence of sharing between father and sons for genes on the X chromosome, the linkage results did not support this hypothesis. No linkage was observed between the X chromosome marker and uric acid concentrations ( $P > 0.05$ ).

One previous attempt has been made to find linkage between polymorphic loci, gout, and hyperuricemia. In

TABLE II. Correlation Between Sex, Age, and BMI kg/m<sup>2</sup> With Uric Acid Concentration

| Relationship | Sex     | Age     | BMI kg/m <sup>2</sup> |
|--------------|---------|---------|-----------------------|
| All subjects | 0.323** | −0.081* | 0.290**               |
| Mother       | N/A     | 0.034   | 0.382**               |
| Fathers      | N/A     | 0.105   | 0.432**               |
| Index case   | 0.230** | −0.104  | 0.336**               |
| Sisters      | N/A     | 0.085   | 0.518**               |
| Brothers     | N/A     | −0.066  | 0.373**               |

N/A = not applicable.

\* $P \leq 0.05$ .

\*\* $P \leq 0.01$ .

TABLE III. Inter- and Intraclass Correlations Among Family Members for Uric Acid Concentration

| Relationship     | n   | Correlation coefficients (r) |
|------------------|-----|------------------------------|
| Mother–father    | 77  | 0.041                        |
| Parent–offspring | 842 | 0.167**                      |
| Sib              | 863 | 0.349**                      |
| Mother–daughter  | 382 | 0.169**                      |
| Mother–son       | 142 | 0.189**                      |
| Father–daughter  | 232 | 0.201**                      |
| Father–son       | 86  | 0.013                        |
| Sister–sister    | 439 | 0.415**                      |
| Sister–brother   | 339 | 0.247**                      |
| Brother–brother  | 85  | 0.295**                      |

Correlation coefficients marked with an \* indicated statistically significant evidence for familial aggregation (\* =  $P < 0.05$ ; \*\* $P < 0.01$ ).



black South Africans, one allele of the HLA system (HLA-B14) was more common in patients with primary gout compared with a control group, but the implications of this observation are unclear [Cassim et al., 1994].

An important question for multigenic traits is the extent to which genes that determine Mendelian disorders also have alleles that contribute to normal quantitative variation. Although two single gene mutations cause gout, neither of these genes appears to influence uric acid concentrations in our families. The placement of our markers relative to these genes makes it unlikely that the lack of support for linkage was due to low marker density or uninformative haplotypes (DXS1062—6 Mb—HPRT1—3.5 Mb—DXS8073; DXS1059—1.3 Mb—PRPS1—6.2 Mb—DXS1212).

Two other studies examined the pattern of family correlations for uric acid concentrations, finding that sons resembled their fathers nearly to the same extent that they resembled their mothers [Brunner et al., 1971; Friedlander et al., 1988]. In neither of these studies was uric acid concentration adjusted for BMI, so the father-son similarity could be secondary to resemblance in weight and height. Additionally, in both reports the sons were children, whereas in the current study the offspring were middle-aged. Because uric acid levels are influenced by sex hormones [Bondy and Rosenberg, 1980], different genes might be involved in uric acid concentration before and after puberty. Additional studies in families with adult children are needed to confirm the lack of father-son similarity found among the families studied here. Most family members have been genotyped for multiple autosomal markers (data not shown). Therefore, a bias in nonpaternity detection is unlikely to account for the lack of father-son similarity.

Environmental influences are present for most complex disorders such as diabetes and hypertension. In the case of gout and hyperuricemia, food selection and alcohol consumption have large effects on final uric acid concentration. While no adoption studies have been conducted, several lines of evidence suggest that a similarity in uric acid concentration between family members is not solely accounted for by similarity in diet. In one study of Israeli children, those living in collective housing (Kibbutz) were similar to their parents in uric acid concentration, although all families studied ate food prepared in a single kitchen [Brunner et al., 1971]. In another study, uric acid concentrations were more similar if adult twins lived together but similarity for twins living apart was still strong [Boyle et al., 1967]. Adoption studies and detailed studies of twins may help resolve the relative contribution of diet and genotype.

Besides sex, an important determinant of uric acid concentration is weight adjusted for height. As BMI increases, so does uric acid concentration, and this relationship is true for both men and women. In the analysis of family resemblance and linkage, the phenotypes were adjusted for BMI, and therefore genes with a pleiotropic effect on BMI and uric acid concentration would have been less likely to be found. However, analysis of uric acid concentrations unadjusted for BMI

displayed no evidence for linkage (data not shown). The mechanism by which plasma uric acid concentration is increased among individuals with elevated BMI is not known, but leptin appears to have a role in the development of hyperuricemia [Fruehwald-Schultes et al., 1999].

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## ELECTRONIC DATABASE INFORMATION

URLs for the data in this article are as follows:

Whitehead Institute, <http://www-genome.wi.mit.edu>  
Genome Database, <http://www.gdb.org>  
Cooperative Human Linkage Database, <http://www.chlc.org>  
Genetic Location Database, <http://cedar.genetics.soton.ac.uk>

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